

Setting up a female genomic reference population for German Holstein

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Abstract

Genomic evaluation for German Holsteins is currently based on a reference population of more than 33,000 Holstein bulls. In order to achieve an even higher accuracy of genomic prediction and implement genomic selection timely also for new traits, routine genotyping of young heifers or lactating cows has started in Germany to set up a female genomic reference population. In 2016 a large-scale genotyping project, **KuhVision**, was started by German breeding organisations with the aim of obtaining 150,000 reference cows within three years. In addition to the traits routinely collected through milk recording or type classification programmes, a set of new traits will be added to the conventional and genomic evaluations: mastitis for udder health, retained placenta and infertility/cycle disturbances representing reproduction, ketosis, milk fever and left-displaced abomasum for metabolism, and several claw health traits. The setup of the large **KuhVision** project based on the experiences gained in two basic research projects. Data recording and genetic evaluation for the novel traits have been established within the research project GKUHplus funded by German Ministry of Agriculture (BMEL). First experiences with a cow reference population come from the research project, **Kuh-L**, founded by the German Ministry of Sciences (BMBF) and breeding organisations. Approximately 20,000 Holstein heifers or cows born in 2011 to 2013 were genotyped from 56 large commercial dairy herds. All female animals from these herds were chosen for the genotyping, without any pre-selection. Accuracy and bias of the female reference population for genomic prediction were assessed based on 11,785 genotyped cows from the **Kuh-L** project. The accuracy and bias of the cow reference population were compared to a reference population of 9,422 Holstein bulls with daughter phenotypes exclusively in Germany. A total of 605 daughter-proven bulls born between 2010 and 2012 were selected as validation animals in the genomic validation study. Despite the low number of reference cows, the cow reference population has reached a reasonably high accuracy and considerably low bias of genomic prediction comparable to the results of the bull reference population. Validation accuracy, squared correlation between candidate genomic proofs (GEBV) and conventional daughter EBV, was for the cow reference population lower, on average 0.07 for three milk production traits, than for the bull reference population. Somatic cell score showed larger difference in validation accuracy, 0.16, between the two reference populations. Regression coefficients of deregressed conventional proofs on the candidate GEBV of the validation bulls were lower for the cow reference population, indicating that inflation of genomic prediction was worse for the cow reference population. It is expected that the accuracy of prediction will improve and the prediction bias will be reduced, when more genotyped cows are added to the reference population. Genomic evaluation and validation will be extended to the newly collected traits. It will be investigated how the bull and cow reference populations should be combined to achieve the highest accuracy and lowest bias of genomic prediction.

Keywords: Genomic evaluation, female reference population, genomic validation